

Patent Application US/07/943,852



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Le, Junming
Vilcek, Jan
Daddona, Peter E.
Ghrayeb, John
Knight, David M.
Siegel, Scott A.

(ii) TITLE OF INVENTION: MONOCLONAL AND CHIMERIC ANTIBODIES
SPECIFIC FOR HUMAN TUMOR NECROSIS FACTOR

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Browdy and Neimark
(B) STREET: 419 Seventh Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0,
Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/670,827
(B) FILING DATE: 18-MAR-1991

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
1 5 10 15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA 48
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly

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107      1              5              10              15
108
109  GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC   96
110  Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
111              20              25              30
112
113  ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA   144
114  Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
115              35              40              45
116
117  AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC   192
118  Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
119              50              55              60
120
121  AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT   240
122  Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
123      65              70              75              80
124
125  GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC   288
126  Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
127              85              90              95
128
129  ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA   321
130  Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
131              100              105
132
133
134  (2) INFORMATION FOR SEQ ID NO:3:
135
136      (i) SEQUENCE CHARACTERISTICS:
137          (A) LENGTH: 107 amino acids
138          (B) TYPE: amino acid
139          (D) TOPOLOGY: linear
140
141      (ii) MOLECULE TYPE: protein
142
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
144
145  Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
146      1              5              10              15
147
148  Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
149              20              25              30
150
151  Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
152              35              40              45
153
154  Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
155              50              55              60
156
157  Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
158      65              70              75              80
159

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160 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
161 85 90 95

162
163 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
164 100 105

166 (2) INFORMATION FOR SEQ ID NO:4:

168 (i) SEQUENCE CHARACTERISTICS:

169 (A) LENGTH: 357 base pairs

170 (B) TYPE: nucleic acid

171 (C) STRANDEDNESS: single

172 (D) TOPOLOGY: linear

174 (ii) MOLECULE TYPE: cDNA

177 (ix) FEATURE:

178 (A) NAME/KEY: CDS

179 (B) LOCATION: 1..357

182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

184 GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA 48

185 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

186 1 5 10 15

188 TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC 96

189 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Ser Asn His

190 20 25 30

192 TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT 144

193 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val

194 35 40 45

196 GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG 192

197 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu

198 50 55 60

200 TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT 240

201 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala

202 65 70 75 80

204 GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT 288

205 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr

206 85 90 95

208 TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA 336

209 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln

210 100 105 110

212 GGC ACC ACT CTC ACA GTC TCC 357

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213 Gly Thr Thr Leu Thr Val Ser

214 115

215

216

217 (2) INFORMATION FOR SEQ ID NO:5:

218

219 (i) SEQUENCE CHARACTERISTICS:

220 (A) LENGTH: 119 amino acids

221 (B) TYPE: amino acid

222 (D) TOPOLOGY: linear

223

224 (ii) MOLECULE TYPE: protein

225

226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

227

228 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

229 1 5 10 15

230

231 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His

232 20 25 30

233

234 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val

235 35 40 45

236

237 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu

238 50 55 60

239

240 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala

241 65 70 75 80

242

243 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr

244 85 90 95

245

246 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln

247 100 105 110

248

249 Gly Thr Thr Leu Thr Val Ser

250 115

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/943,852

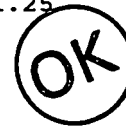
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ORIGINAL TEXT

29 Response Exceeds Line Limitations

Version #1.25



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PATENT APPLICATION US/07/943,852

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/943,852

DATE: 09/21/92
TIME: 12:01:05

LINE ORIGINAL TEXT

CORRECTED TEXT